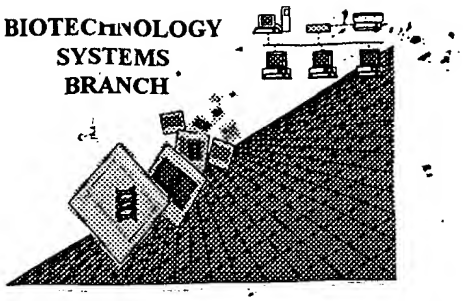
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/911,261

Source: OIPE

Date Processed by STIC: 8/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/911,261

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ✓ Variable Length — Sequence(s) 1-2 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ✓ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown.". Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001
TIME: 15:07:46

Does Not Comply
Corrected Diskette Needed
pp 1, 3, 6-8

Input Set : A:\109845-130.txt
Output Set: N:\CRF3\08012001\I911261.raw

```
      2 <110> APPLICANT: Sera, Takashi
      4 <120> TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
      6 <130> FILE REFERENCE: 109846-130
C-->  8 <140> CURRENT APPLICATION NUMBER: US/09/911,261
C-->  8 <141> CURRENT FILING DATE: 2001-07-23
      8 <150> PRIOR APPLICATION NUMBER: US 60/220,060
     10 <151> PRIOR FILING DATE: 2000-07-21
     12 <160> NUMBER OF SEQ ID NOS: 69
     14 <170> SOFTWARE: PatentIn version 3.0
```

ERRORED SEQUENCES

```
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 28
     18 <212> TYPE: PRT
     19 <213> ORGANISM: Artificial Sequence
     21 <220> FEATURE:
     22 <223> OTHER INFORMATION: Zinc finger domain.
     24 <220> FEATURE:
     25 <221> NAME/KEY: VARIANT
     26 <222> LOCATION: (1)..(28)
     27 <223> OTHER INFORMATION: Amino acids 1-3, 8-19 and 25-28 are Xaa wherein Xaa = any
amino
     28       acid.
     30 <220> FEATURE:
     31 <221> NAME/KEY: VARIANT
     32 <222> LOCATION: (5)..(6)
     33 <223> OTHER INFORMATION: Amino acid 5 is Xaa wherein Xaa = any amino acid, amino acids
     34       and 6 together represent from 2 to 4 amino acids in length.
     36 <220> FEATURE:
     37 <221> NAME/KEY: VARIANT
     38 <222> LOCATION: (21)..(23)
     39 <223> OTHER INFORMATION: Amino acid 21 is Xaa wherein Xaa = any amino acid, amino
acids
     40       21-23 together represent from 3 to 5 amino acids in length.
E--> 42 <400> SEQUENCE: 0
W--> 44 Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     45 1               5                  10                  15
W--> 47 Xaa Xaa Xaa His Xaa Xaa Xaa His Xaa Xaa Xaa Xaa
     48          20                  25
     51 <210> SEQ ID NO: 2
     52 <211> LENGTH: 28
     53 <212> TYPE: PRT
     54 <213> ORGANISM: Artificial Sequence
     56 <220> FEATURE:
     57 <223> OTHER INFORMATION: Zinc finger domain.
```

5

Xaa can only represent a single amino acid - variable length not permitted - see item 5 on Error Summary Sheet

same error

see p-6

59 <220> FEATURE:
60 <221> NAME/KEY: VARIANT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001
TIME: 15:07:46

Input Set : A:\109845-130.txt
Output Set: N:\CRF3\08012001\I911261.raw

```
     61 <222> LOCATION: (1)..(28)
     63 <223> OTHER INFORMATION: Amino acids 1-3, 8-12, 14, 17-18 and 25-28 are Xaa wherein
Xaa =
     64       any amino acid.
     66 <220> FEATURE:
     67 <221> NAME/KEY: VARIANT
     68 <222> LOCATION: (5)..(6)
     69 <223> OTHER INFORMATION: Amino acid 5 is Xaa wherein Xaa = any amino acid, amino acids
5
     70       and 6 together represent from 2 to 4 amino acids in length.
     72 <220> FEATURE:
     73 <221> NAME/KEY: VARIANT
     74 <222> LOCATION: (21)..(23)
     75 <223> OTHER INFORMATION: Amino acid 21 is Xaa wherein Xaa = any amino acid, amino
acids
     76       21-23 together represent from 3 to 5 amino acids in length.
     78 <220> FEATURE:
     79 <221> NAME/KEY: VARIANT
     80 <222> LOCATION: (13)..(13)
     81 <223> OTHER INFORMATION: Amino acid 13 is Xaa wherein Xaa = Z-1 wherein Z-1 = Arg or
Lys,
     82       Gln or Asn, Thr, Met, Leu or Ile, or Glu or Asp.
     84 <220> FEATURE:
     85 <221> NAME/KEY: VARIANT
     86 <222> LOCATION: (15)..(15)
     87 <223> OTHER INFORMATION: Amino acid 15 is Xaa wherein Xaa = Z2 wherein Z2 = Ser or
Arg,
     88       Asn Gln, Thr, Val or Ala, or Asp or Glu.
     90 <220> FEATURE:
     91 <221> NAME/KEY: VARIANT
     92 <222> LOCATION: (16)..(16)
     93 <223> OTHER INFORMATION: Amino acid 16 is Xaa wherein Xaa = Z3 wherein Z3 = His or
Lys,
     94       Asn or Gln, Ser, Ala, or Val, or Asp or Glu.
     96 <220> FEATURE:
     97 <221> NAME/KEY: VARIANT
     98 <222> LOCATION: (19)..(19)
     99 <223> OTHER INFORMATION: Amino acid 19 is Xaa wherein Xaa = Z6 wherein Z6 = Arg or
Lys,
    100       Gln or Asn, Thr, Tyr, Leu, Ile or Met, or Glu or Asp.
E--> 102 <400> SEQUENCE: 0
W--> 104 Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    105 1               5                  10                  15
W--> 107 Xaa Xaa Xaa His Xaa Xaa Xaa His Xaa Xaa Xaa Xaa
    108             20                  25
    111 <210> SEQ ID NO: 3
    112 <211> LENGTH: 196
    113 <212> TYPE: PRT
    114 <213> ORGANISM: Artificial Sequence
    116 <220> FEATURE:
    117 <223> OTHER INFORMATION: Zinc finger protein.
E--> 119 <400> SEQUENCE: 0
    121 Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
```

```
122 1               5                   10                  15
124 Cys Gly Lys Val Tyr Gly Gln Ser Ser Asp Leu Gln Arg His Leu Arg
125             20                  25                  30
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001
TIME: 15:07:46

Input Set : A:\109845-130.txt
Output Set: N:\CRF3\08012001\I911261.raw

```
127 Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
128         35                  40                  45
130 Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
131     50                  55                  60
133 Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
134 65                  70                  75                  80
136 Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
137                 85                  90                  95
139 Asp Gly Gly Gly Ser Gly Lys Lys Lys Gln His Ile Cys His Ile Gln
140             100                 105                 110
142 Gly Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu
143         115                 120                 125
145 Arg Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys
146     130                 135                 140
148 Gly Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr
149 145                 150                 155                 160
151 His Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe
152                 165                 170                 175
154 Met Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys
155             180                 185                 190
157 Lys Gly Gly Ser
158         195
```

delete extra bracket

<400>) 1 same error as Seq. 2, Seq 3

Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

FYI

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

<211> 45
<212> DNA
<213> Artificial Sequence (PCR Primer) This goes on <2237 line, not <2137 line (see item 10 on Error Summary Sheet)
<2207
<2237
<400> 54
ttcagggcgg tctctcggct tctcgccagt gtgagtacgc tgatg 45

<400> 69

Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Xaa Ser Xaa Xaa
1 5 10 15

Leu Ser Xaa His Gln Arg Thr His Thr Gly Glu Lys
20 25

109845-130.ST25

Page 1

Deleti

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001
TIME: 15:07:47

Input Set : A:\109845-130.txt
Output Set: N:\CRF3\08012001\I911261.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:102 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:119 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1151 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1151 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:1351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:1389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:1392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69